Biodiversity Data Journal 14: e177603
doi: 10.3897/BDJ.14.e177603

Taxonomy & Inventories

Dictyolimon gilesii (Plumbaginaceae), a new generic record to China, with special reference to its first plastome

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Academic editor: Gianniantonio Domina

Received: 10 Nov 2025 | Accepted: 15 Feb 2026 | Published: 04 Mar 2026

Citation: Zhang Y, Zhang K, Huang W, Abdusalam A (2026) *Dictyolimon gilesii* (Plumbaginaceae), a new generic record to China, with special reference to its first plastome. Biodiversity Data Journal 14: e177603. https://doi.org/10.3897/BDJ.14.e177603

Abstract

Background

Dictyolimon (Plumbaginaceae, *Caryophyllales*) is a small genus with three currently accepted species. Nevertheless, its distribution remains poorly known, with records confined to Afghanistan, Pakistan and India (Kashmir). During recent fieldwork on the eastern Pamir Plateau in China, we discovered a distinctive perennial herb, identifiable as *Dictyolimon gilesii*. This species is characterised by densely rosulate, coriaceous, obovate or spatulate leaves; spikelets with 3–10-flowers (typically 6), sessile; bifid petals; a pubescent calyx tube; styles free from the base; and oblique-capitate stigmas. This finding represents the first record of the genus *Dictyolimon* in China. Phylogenetic analysis, based on the ITS and *trn*Y-*trn*T loci, further support our morphology-based conclusions. Additionally, we report the first complete plastome of *Dictyolimon*, which is 152,328 bp in length and contains 121 functional genes.

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New information

Dictyolimon gilesii new to China.

Keywords

chloroplast genome, ITS, Pamir Plateau, *trn*Y-*trn*T, Xinjiang

Introduction

The East Pamir Plateau (located in China) harbours unique plant resources, with 963 recorded taxa (Yang et al. 2008). Its distinctive habitat has continually attracted botanical interest. In recent years, numerous species new to China or science have been discovered in this region, such as *Astragalus dignus* Boriss (Zhai et al. 2010), *Delphinium afghanicum* Rechinger (Li et al. 2019), *Didymophysa fedtschenkoana* Regel (Yang et al. 2024), *Gagea chenghsii* J.Qiu & D.Y.Tan (Lin 2023), *Saussurea khunjerabensis* Y.S.Chen (Li et al. 2022) and *Sisymbriopsis schugnana* Botsch. & Tzvelev (Chen et al. 2019). Although these studies have significantly enhanced our understanding of the regional flora, knowledge of the plant diversity in the East Pamir Plateau remains limited, as many areas are still unexplored.

To enhance our understanding of plant diversity in the Pamir Plateau in China, we conducted a field survey in this region (Abdusalam et al. 2024). In 2024, we discovered an intriguing plant, characterised by densely rosulate, thick, coriaceous, obovate or spatulate leaves with an aculeate-mucronate apex, which we tentatively referred to as either *Limonium* or *Dictyolimon*. However, the absence of flowers prevented definitive species identification. In 2025, we observed the inflorescence of this species, which exhibited the following features: (1) spikelets loosely and subdistichously arranged along the branches, forming elongated, interrupted spicate clusters; (2) spikelets 3–10-flowered (typically 5–6), sessile; (3) a pubescent calyx tube; (4) bifid petals; and (5) styles free from the base with oblique-capitate stigmas. These morphological traits closely match the description of *Dictyolimon gilesii*. Phylogenetic analysis, based on ITS and *trn*Y-*trn*T loci, further confirmed that this species belongs to the genus *Dictyolimon*, representing the first record of this genus in China.

Plastomes are characterised by relatively small genome sizes, conservative gene content and a moderate evolutionary rate (Xu et al. 2025). Recently, plastomes have become an indispensable source of molecular data and are widely employed in studies on the taxonomy and evolution of the Plumbaginaceae (e.g. Darshetkar et al. 2021, Zhao YJ et al. 2023). Here, we report the first plastome of *Dictyolimon*, which may provide valuable insights into the evolutionary history and phylogenetic relationships of this genus.

The primary objectives of this study are to: (1) report the first occurrence of the genus *Dictyolimon* in China; (2) investigate the phylogenetic relationships of the Chinese species *Dictyolimon gilesii* and (3) present the first complete plastome of *Dictyolimon*.

Materials and methods

Taxon sampling

The plant material was collected from Xigelu Township in Tashekuergan Tajik Autonomous County, Kashi Prefecture, Xinjiang Uygur Autonomous Region, China. The voucher specimen (*Zhang et al. KSU-ERCP-2025-3329*) was deposited in the Herbarium of Kashi University and was utilised for phylogenetic analyses. The sampled ingroup and outgroup taxa are listed in Table 1.

Table 1.

Voucher information and GenBank accession numbers of ITS and *trn*Y-*trn*T sequences used in this study; new sequences in bold. "—" means data missing.

Species	**Location**	**Vouchers (herbarium code)**	***nr* DNA ITS**	***trn*Y-*T***
Acantholimon acerosum (Willd.) Boiss.	Turkey	*Eren s.n.* (W 2014-12433)	LC153805	LC153954
Acantholimon acerosum (Willd.) Boiss.	Turkey	*Aedo et al. 6249* (MA 688508)	LC153806	LC153955
Acantholimon acmostegium Boiss. & Buhse	Iran	*Kazempour-Osaloo & Moharrek s.n.* (TMUH 92351)	LC153807	LC153956
Acantholimon acmostegium Boiss. & Buhse	Iran	*Assadi 84464* (TARI)	AB979532	AB979600
Acantholimon ahangarense Rech.f. & Schiman-Czeika	Afghanistan	*Rechinger 18860* (W 1975-0013927)	LC153808	LC153957
Acantholimon alatavicum Bunge	Uzbekistan	*Vašák s.n.* (MA 642281)	LC153809	LC153958
Acantholimon austroiranicum Rech.f. & Schiman-Czeika	Iran	*Mirtadzadini 83216* (TARI)	AB979538	AB979605
Acantholimon balchanicum Korovin	Turkmenistan	*Nikitin s.n.* (W 1985-0007275)	LC153816	LC153965
Acantholimon sirchense Assadi & Mirtadz.	Iran	*Mirtadzadini s.n.* (SHBU 1266)	AB979581	AB979640
Acantholimon ulicinum (Willd. ex Schult.) Boiss.	Greece	*Merxmüller & Podlech 30886* (M 0276189)	LC153920	LC154036
Acantholimon venustum Boiss.	Turkey	*Aldasoro et al. 2724* (MA 689899)	LC153925	LC154040
Acantholimon zaprjagaevii Lincz.	Afghanistan	*Podlech 16364* (M 0276224)	LC153931	LC154045
Armeria maderensis Lowe	Portugal	*Piñeiro 112RP10* (MA)	LC153932	LC154046
Armeria maritima (Mill.) Willd.	Iran	Cultivated National Botanical Garden Iran	AB979588	AB979647
Armeria pungens (Brot.) Hoffmanns. & Link	Portugal	*Nieto Feliner 4457GN* (MA)	LC153933	LC154047

Species	Location	Vouchers (herbarium code)	*nr* DNA ITS	*trnY-T*
Armeria villosa subsp. longiaristata (Boiss. & Reut.) Nieto Fel.	Spain	*Nieto Feliner 4255GN* (MA)	LC153934	LC154048
Armeria welwitschii Boiss.	Iran	Cultivated National Botanical Garden Iran	AB979589	AB979648
Bamiania pachycorma (Rech.f.) Lincz.	Afghanistan	*Hedge & Wendelbo 4103* (E)	LC153935	LC154049
Bukiniczia cabulica (Boiss.) Lincz.	Afghanistan	*Podlech 21781* (M 0276239)	LC153936	LC154050
Bukiniczia cabulica (Boiss.) Lincz.	Afghanistan	*Alpay s.n.* (MSB 006138)	LC153937	LC154051
Cephalorhizum coelicolor (Rech.f.) Rech.f.	Afghanistan	*Anders 9314* (MSB 006131)	LC153938	LC154052
Cephalorhizum coelicolor (Rech.f.) Rech.f.	Afghanistan	*Podlech 11313* (MSB 006132)	LC153939	LC154053
Chaetolimon setiferum (Bunge) Lincz.	Kazakhstan	*Neustruyeva et al. s.n.* (M)	LC153940	——
Dictyolimon griffithii (Aitch. & Hemsl.) Rech.f.	Afghanistan	*Podlech 16138* (MSB 006130)	LC153941	——
Dictyolimon macrorrhabdos (Boiss.) Rech.f.	Afghanistan	*Podlech 30260* (MSB 006135)	LC153942	LC154054
Dictyolimon macrorrhabdos (Boiss.) Rech.f.	Afghanistan	*Podlech 18032* (MSB 006134)	LC153943	LC154055
Dyerophytum socotranum (Balf.f.) J.R.Edm., M.Malekm. & Koutr.	Yemen	*Miller et al. 10300* (E 0035670)	LC153944	LC154056
Gladiolimon speciosissimum (Aitch. & Hemsl.) Mobayen	Afghanistan	*Podlech 16945* (MSB 006125)	LC153945	LC154057
Gladiolimon speciosissimum (Aitch. & Hemsl.) Mobayen	Afghanistan	*Amin 74* (MSB 006126)	LC153946	LC154058
Goniolimon italicum Tammaro, Pignatti & Frizzi	Italia	*Conti s.n.*	LC217873	——
Goniolimon speciosum (L.) Boiss.	Russia	*Castroviejo 14315SC* (MA 614247)	LC217874	——
Limonium axillare (Forssk.) Kuntze	Iran	*Maassoumi & Abu Hamzeh 52016* (TARI)	LC153947	LC154059
Limonium carnosum (Boiss.) Kuntze	Iran	*Assadi 79082* (TARI)	LC153948	LC154060
Limonium carnosum (Boiss.) Kuntze	Iran	*Kazempour-Osaloo s.n.* (TMUH 92360)	LC153949	LC154061
Limonium gmelinii (Willd.) Kuntze	Iran	*Memariani & Zanguei 41461* (FUMH)	AB979591	AB979650
Limonium iranicum (Bornm.) Lincz.	Iran	*Memariani & Akhani 39323* (FUMH)	AB979592	AB979651
Limonium meyeri (Boiss.) Kuntze	Iran	*Kazempour-Osaloo s.n.* (TMUH 89213)	AB979593	AB979652
Limonium nudum (Boiss. & Buhse) Kuntze	Iran	*Assadi & Maassoumi 21019* (TARI)	LC153950	LC154062

Species	Location	Vouchers (herbarium code)	*nr* DNA ITS	*trnY-T*
Limonium reniforme (Girard) Lincz.	Iran	*Joharchi & Zanguei 1484* (FUMH)	AB979594	AB979653
Limonium sogdianum (Popov) Ikonn.-Gal.	Iran	*Joharchi 34168* (FUMH)	AB979595	AB979654
Limonium suffruticosum (L.) Kuntze	Iran	*Joharchi 35188* (FUMH)	LC153952	AB979655
Plumbago europaea L.	Iran	*Zanguei 38466* (FUMH)	AB979599	AB979659
Popoviolimon turcomanicum (Popov) Lincz.	Iran	*Joharchi & Zanguei 36270* (FUMH)	AB979590	AB979649
Popoviolimon turcomanicum (Popov) Lincz.	Iran	*Faghihnia & Zanguei 28978* (FUMH)	JX983658	——
Psylliostachys beludshistanica Roshk.	Iran	*Faghihnia & Zanguei 18122* (FUMH)	AB979596	AB979656
Psylliostachys leptostachya (Boiss.) Roshk.	Iran	*Joharchi & Zanguei 14525* (FUMH)	AB979597	AB979657
Psylliostachys spicata (Willd.) Nevski	Iran	*Zanguei 34446* (FUMH)	AB979598	AB979658
Psylliostachys suvorovii (Regel) Roshk.	Austria	Cultivated Insbruck Botanical Garden	AJ132446	——
Vassilczenkoa sogdiana (Lincz.) Lincz.	Afghanistan	*Podlech 21130* (M 0276244)	——	LC154063
Limonium vulgare Hill.	Spain	*Roselló JAR 96085*	AJ222839	——

Morphological study

Species photographs and habitat were taken using a digital camera. The Deep Focus Small Specimen Digital Imaging System was employed to photograph the dissected structures. Morphometric measurements and descriptions were derived from the only flowering individual observed and more than 30 flowers from this specimen were measured and dissected.

DNA extraction, sequencing, genome assembly and annotation

Sample preparation and DNA extraction followed protocols used in previous studies (Huang et al. 2019). High-quality genomic DNA from each sample was used for the whole genome sequencing to obtain paired-end 150 bp raw reads on the Novaseq-SE50 platform, according to the manufacturer's procedures and about 5.2 Gb of sequences were accumulated. Raw reads with a Phred score lower than 30 were removed, retaining high-quality sequences for nuclear DNA and complete circular organelle genome assembly using the GetOrganelle v. 1.7.7.1 (Jin et al. 2020). The assembly graph viewer Bandage (Wick et al. 2015) was used to visualise the assemblies. Genomes were automatically annotated with CPGAVAS2 (Shi et al. 2019) and subsequently refined using Geneious v.11.0.3 (Kearse et al. 2012), with *Limonium sinense* (accession number: MN599096) as the reference plastome. Circular organelle genomes maps were drawn using OrganellarGenome DRAW (Lohse et al. 2013). The assembled nuclear data were

aligned with published data using *Dictyolimon macrorrhabdos* as a reference (ITS accession number: LC153943) in Geneious v.11.0.3 (Kearse et al. 2012) and then annotated and extracted. The *trn*Y-*trn*T locus was extracted from the chloroplast genome. Newly-sequenced data have been deposited in the GenBase (Bu et al. 2024) in the National Genomics Data Center (CNCB-NGDC Members and Partners 2022), with accession numbers: C_AA126288.1: plastome; and C_AA126289.1: ITS).

Phylogenetic analyses

All the sequences were aligned using MAFFT v.7.311 (Katoh and Standley 2013) and ambiguous alignment regions were trimmed using trimAl v.1.2 (Capella-Gutiérrez et al. 2009) Absent data were coded as missing. Maximum Likelihood (ML) analyses were performed in IQtree v.2.0.6 (Minh et al. 2020) with the sampling repeated 1000 times. The best-fitting substitution model (TIM3e+G4 for the ITS-partition and K3Pu+F+G4 for the *trn* Y-*trn*F-partition) was selected by ModelFinder (Chernomor et al. 2016, Kalyaanamoorthy et al. 2017), according to the Bayesian Information Criterion (BIC). For Bayesian Inference analyses, MrBayes 3.2.6 (Ronquist et al. 2012) was used to run and construct phylogenetic trees with 3,000,000 replicates, with trees sampled every 1000 generations. GTR+I+G was found to be the best-fit model for ITS-partition and GTR+G for the *trn*Y-*trn*F, according to the Akaike Information Criterion (AICc). Markov Chain Monte Carlo (MCMC) was run independently twice with one cold and three hot chains. The posterior distribution of trees was summarised by the 50% majority-rule consensus tree after discarding the first 25% of samples as burn-in.

Data resources

Phylogenetic results

The aligned two-loci dataset included 1,479 characters: *trn*Y-*trn*F, 867 bp; and ITS, 622 bp. Of the 14,79 aligned nucleotides, 800 were constant sites, 134 were singleton sites and 545 were parsimony-informative sites. Both ML and BI analyses generated almost identical trees with strong support for most nodes. The ML topology tree with bootstrap (BS) and posterior probability (PP) values (BS_{ML} and PP_{BI}, respectively) is shown in Fig. 1.

In the phylogenetic analyses (Fig. 1), all subfamily Limonioideae species formed a well-supported clade (BS_{ML}=100, PP_{BI}=1). Phylogenetic results indicated that the newly-sequenced Chinese accession deeply nested within the genus *Dictyolimon* and formed a well-supported clade with two Afghani *D. macrorrhabdos* accessions and one *D. griffithii* accession (BS_{ML}=99, PP_{BI}=1).

Features of plastome

The plastome of *Dictyolimon gilesii* is 152,328 bp in length (Fig. 2). It exhibits a quadripartite structure with a large single-copy (LSC) region of 81,137 bp, a small single-

copy (SSC) region of 13,221 bp and two inverted repeats (IRs) that are 28,985 bp. The plastome has a nucleotide composition of adenine 36.7% (A), 31.6% thymine (T), 16.6% cytosine (C) and 15.1% guanine (G), resulting in an overall GC content of 31.7%. The plastome contains a total of 121 functional genes, including 78 protein-coding genes, eight ribosomal RNAs (rRNA) and 35 transfer RNAs (tRNA). There are 17 intron-containing genes, with 15 genes containing one intron and both the *ycf*3 and *rps*12 genes containing two introns.

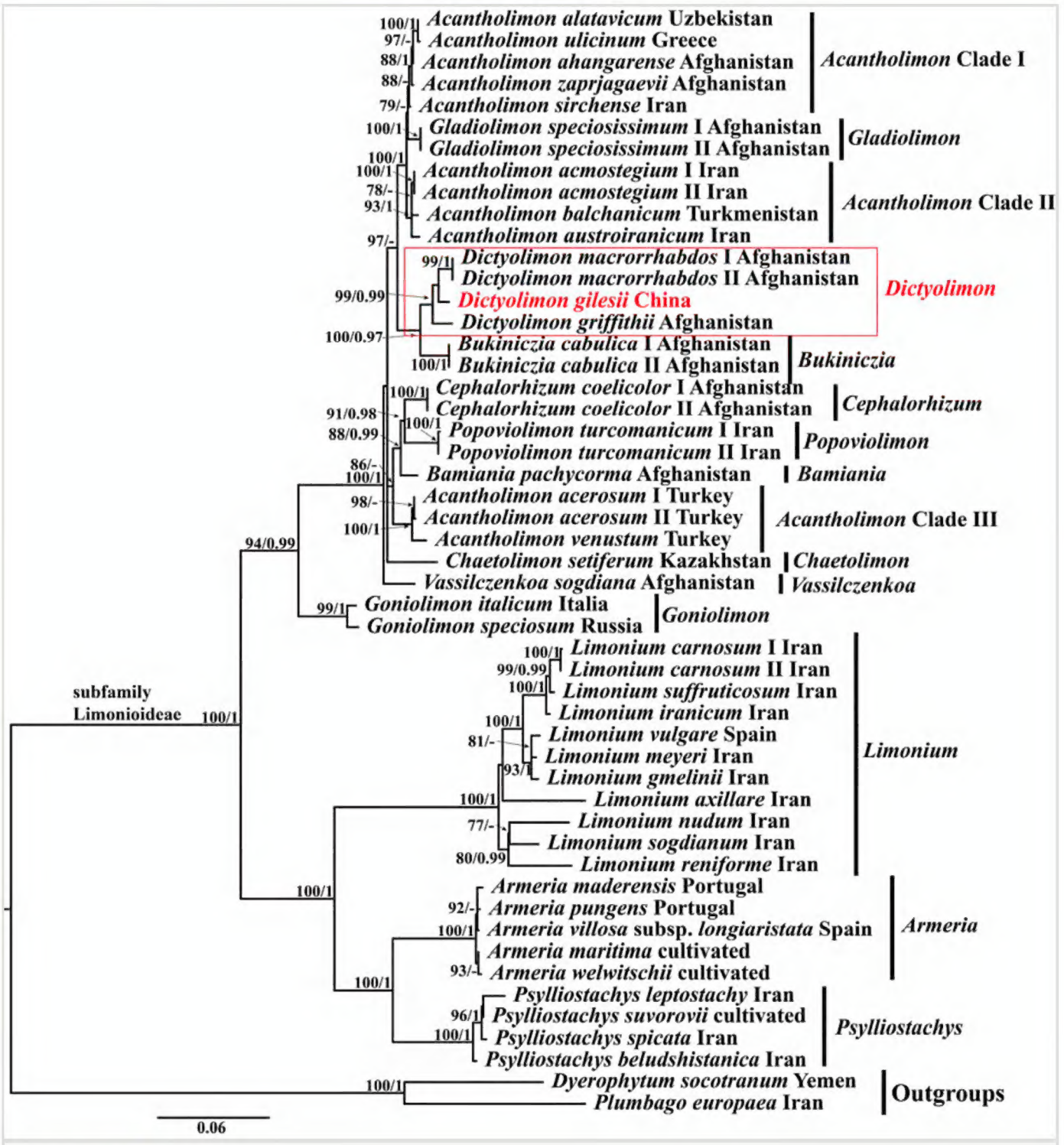

Figure 1. doi

Phylogenetic tree of some Plumbaginaceae species inferred from the combined dataset (ITS and *trn*Y-*trn*T loci). The topology derived from the ML tree is shown. ML bootstrap values are shown on the left and Bayesian posterior probability values on the right. The newly-sequenced Chinese accession is coloured red.

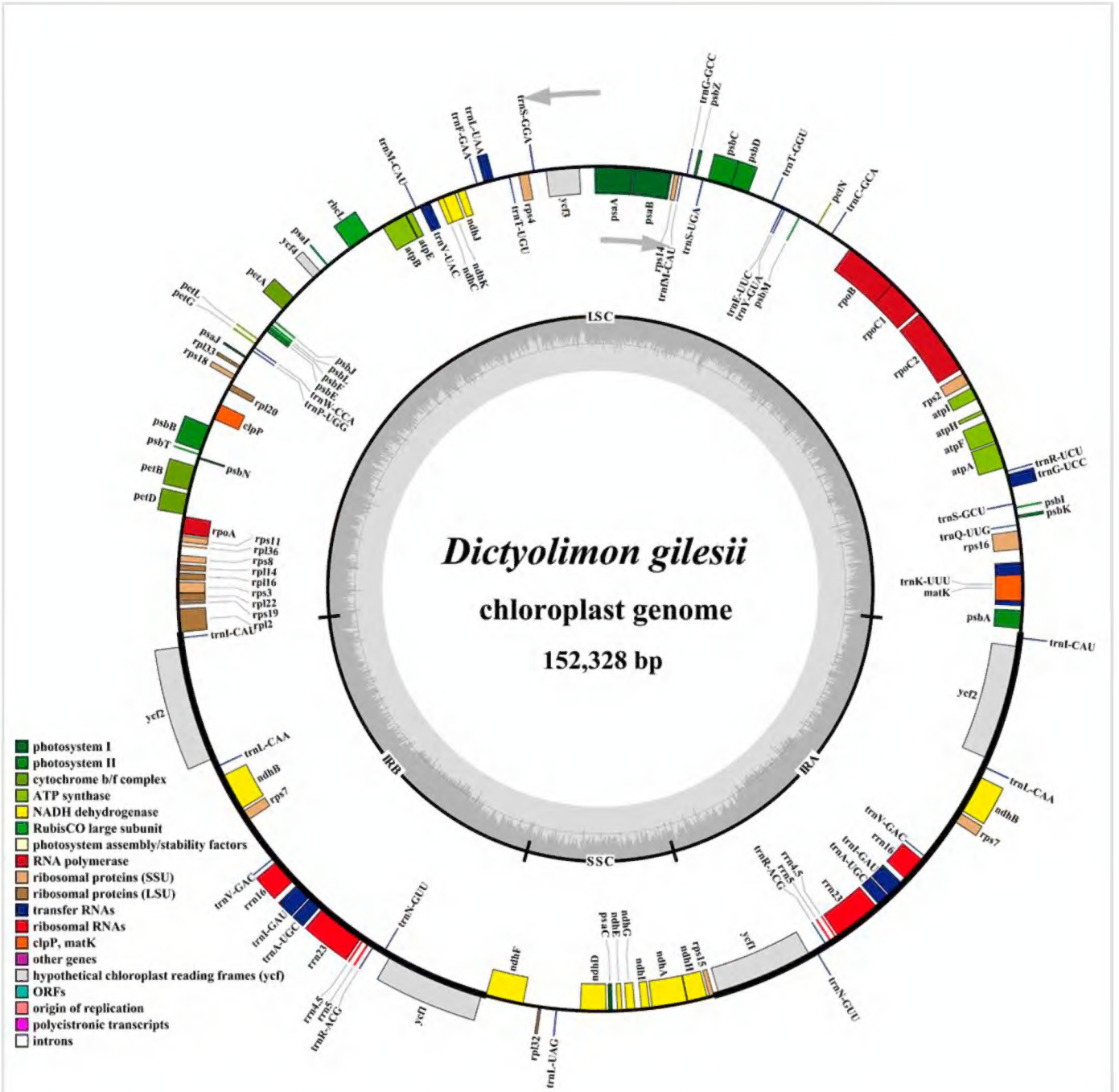

Figure 2. doi

Circular genome map of the chloroplast genome of *Dictyolimon gilesii*. Genes shown on the inside of the circle are transcribed clockwise, genes on the outside are transcribed counterclockwise.

Taxon treatment

Dictyolimon gilesii (Hemsl.)

Nomenclature

Dictyolimon gilesii (Hemsl.) Rech.f., Flora Iranica 108: 22. 1974 (Figs. 3–4)

≡ *Statice gilesii* Hemsl., Hooker's Icones Plantarum.18: tab. 1737. 1888

HOLOTYPE: Hab. Shoghot, at 1828 to 2133 m elev., south of Hindu Kush; Gilgit Expendition, Dr. Giles.(K [digital image!]).

Material

a. country: China; stateProvince: Xinjiang Uygur Autonomous Region; county: Kashi Prefecture, Tashekuergan Tajik Autonomous County; municipality: Kekexiluge Township; verbatimElevation: 2472 m; verbatimLatitude: 37°50′14.04″ N; verbatimLongitude: 75°42′22.18″ E; verbatimEventDate: 26 July 2025; catalogNumber: *KSU-ERCP-2025-3329*; occurrenceRemarks: Herbarium of Kashi University; recordedBy: Yuejuan Zhang; Kai Zhang; Mierkamili Maimaiti

Description

Perennial herb, ca. 25 cm tall, glabrous, glaucous, minutely lepidote. Tap-rooted. Leaves densely rosulate, thick, coriaceous, obovate or spatulate, ca. 2.5–6.3 cm long, apex aculeate-mucronate. Scape solitary, flexuous, usually simple, sometimes with 2–3 short lateral branchlets, with flowers at or below the middle. Spikelets loosely subdistichously arranged along the branches, forming long interrupted spicate clusters. Spikelets 3–10-flowered (usually 5–6-flowered), sessile. Bracts and bracteoles similar, broad and short, almost entirely scarious-hyaline; outer bract shorter. Calyx shortly 10-lobed, tube strongly 10-ribbed, pubescent. Petals 5, bifid. Corolla persistent after anthesis. Stamens 5 opposite the corolla lobes. Filaments linear, widened in the lower part. Ovary glabrous. Styles free from the base, stigmas oblique-capitate. Pericarp dry, membranous, 5–striate, apex easily deciduous. One seed in each calyx tube, seed coat dark brown to black, longitudinally rugose-sulcate (Figs 3, 4).

Distribution

Dictyolimon gilesii is previously known only from Pakistan (Hooker 1888) and Afghanistan (https://records.data.kew.org/occurrences/8a8ba91b-429b-4b84-8d10-069781faaa12?lang=zh-CN). In China, this species is known only from the eastern Pamir Plateau, Xinjiang Uygur Autonomous Region.

Discussion

Dictyolimon gilesii is characterised by the following combination of morphological features: (1) a perennial herbaceous habit (Fig. 3A; Hooker (1888)); (2) leaves densely rosulate, thick, coriaceous, obovate or spatulate, 2.5–6.3 cm long, with an aculeate-mucronate apex (Fig. 3D and E; Hooker (1888)); (3) spikelets 3–10-flowered (typically 6) and sessile (Fig. 4A; Hooker (1888)); (4) bifid petals, styles free from the base and oblique-capitate stigmas (Fig. 4C; Rechinger and Schiman-Czeika (1974)); (5) a glabrous ovary (Fig. 4C; Hooker (1888)); and (6) a pubescent calyx tube (Fig. 4A; Hooker (1888)).

Plumbaginaceae Juss., a nearly cosmopolitan family in the order *Caryophyllales*, exhibits its greatest species diversity in the Northern Hemisphere (Malekmohammadi et al. 2024), particularly across the Mediterranean and Irano-Turanian Regions, as well as in southern

Africa, southern South America and western Australia (Hernández-Ledesma et al. 2015). The family is predominantly composed of halophytes and psammophytes that inhabit saline or coastal environments, along with a substantial clade of cold-adapted orophytes restricted to arid montane regions (Malekmohammadi et al. 2024). *Dictyolimon* belongs to a clade that is distinctly characterised by its non-halophytic ecology (Caperta et al. 2020). We discovered this species at the base of high mountains in a perennially arid region, which represents the only known distribution area of *Dictyolimon* in China.

Figure 3. doi

Dictyolimon gilesii (Hemsl.) Rech.f. **A** habitat and plant; **B** Inflorescence; **C** calyx; **D-E** leaves; **F** roots.

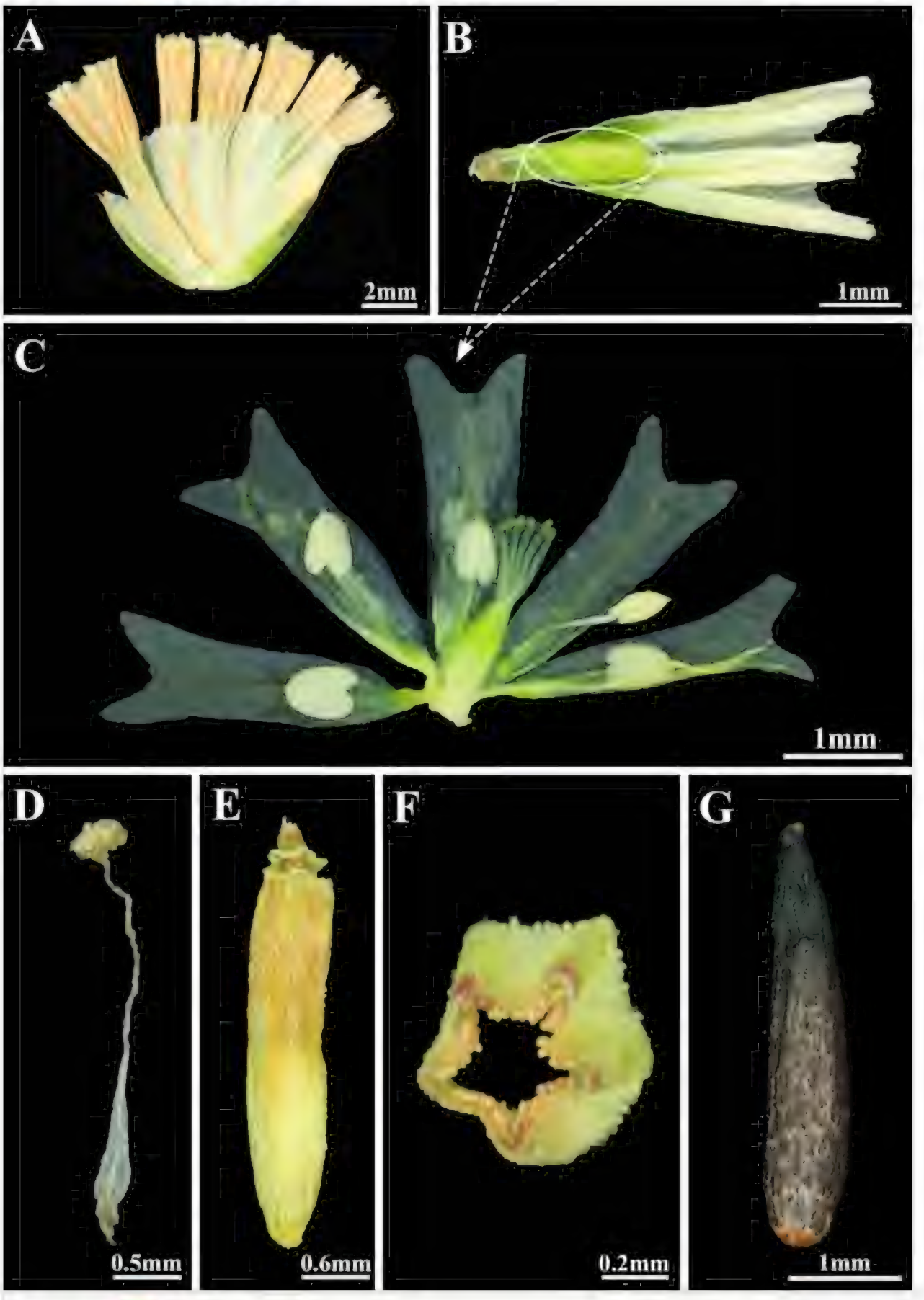

Figure 4. doi

Dictyolimon gilesii (Hemsl.) Rech.f. **A** spikelet with six florets; **B** corolla enclosed by calyx; **C** dissected and spread-open corolla, showing the bract, pistil, stamens and petals; **D** stamen; **E** pericarp; **F** transverse section of pericarp; **G** seed.

The genus *Dictyolimon* currently comprises three accepted species worldwide: *D. gilesii*, *D. griffithii* (Aitch. & Hemsl.) Rech.f. and *D. macrorrhabdos* (Boiss.) Rech.f. While *D. gilesii* and *D. griffithii* are often difficult to distinguish, a primary diagnostic difference lies in the number of flowers per spikelet: *D. gilesii* typically bears 6-flowered spikelets (Fig. 4A;

Hooker (1888)), whereas those of *D. griffithii* bears only one to two flowers (Rechinger and Schiman-Czeika 1974). The tree topology supports the classification of the *D. accession* from Xinjiang Province within *D. macrorrhabdos* (Fig. 1). Morphologically, *D. gilesii* can be easily confused with *D. macrorrhabdos*. However, it can be distinguished by the following characteristics: (1) *D. gilesii* has spikelets with typically six flowers (Fig. 4 A; Koie and Rechinger (1963)), compared to the 3–5 flowers in *D. macrorrhabdos* (Rechinger and Schiman-Czeika 1974); and (2) the calyx tube is pubescent in *D. gilesii* (Fig. 4A; Hooker (1888)), but the calyx is glabrous or sparsely papillate along the ribs in *D. macrorrhabdos* (Rechinger and Schiman-Czeika 1974).

Dictyolimon is morphologically closest to *Bukiniczia* (Moharrek et al. 2017). Notably, our results revealed that these two genera form sister groups (Fig. 1), consistent with previous phylogenetic studies (Moharrek et al. 2017; Koutroumpa et al. 2018). Interestingly, Moharrek et al. (2017) proposed merging eight genera, including *Dictyolimon*, into *Acantholimon*, suggesting a broad circumscription of *Acantholimon* due to the non-monophyly of the species within this genus. Furthermore, our results demonstrate that *Acantholimon* is divided into three clades (Fig. 1), underscoring the need for detailed phylogenetic and taxonomic studies within the *Acantholimon s.l.*

Acknowledgements

We thank the Taxkorgan Wildlife Nature Reserve of Xinjiang Uygur Autonomous Region for issuing the sampling permit; Maimaitiaili from the Wildlife Conservation Station of the Kashi Forestry and Grassland Bureau for his assistance. The research was funded by the National Natural Science Foundation of China (Grant numbers 32460261 and 32500183), the Project for the Collection and Conservation of Important Wild Plant Germplasm Resources in southern Xinjiang (grant numbers WGB-2507) and the Kashi University Innovation Team Construction Project.

Author contributions

Conceptualisation: W.Z.H. and A.A.; methodology: W.Z.H., Y.J.Z. and A.A.; software: W.Z.H.; Investigation: Y.J.Z., A.A. and K.Z; Resources: A.A., W.Z.H. and K.Z.; Data Curation: W.Z.H.; Writing–Original Draft Preparation: Y.J.Z.; Writing–Review and Editing: W.Z.H. and A.A.; Visualisation: W.Z.H., A.A. and Y.J.Z.; Supervision: W.Z.H and A.A.; Project Administration: A.A. and W.Z.H.; Funding Acquisition: A.A. and W.Z.H.

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